

IN THE CLAIMS

Please cancel Claim 3, 17, and 24.

Please substitute the following Claims for the previously pending Claims.

- B1
1. (AMENDED) A method for identifying the presence of a nucleic acid target in a sample by determination of structure formation with said nucleic acid target, comprising the steps of:
- a) providing:
 - i) a sample suspected of having a folded target having a deoxyribonucleic acid sequence comprising one or more double stranded regions, and one or more single stranded regions, and further comprising two or more non-contiguous portions, and one or more intervening regions; and
 - ii) one or more bridging oligonucleotide probes complementary to said two or more non-contiguous portions of said folded target; and
 - b) mixing said folded target and said one or more probes under conditions such that said probe hybridizes to said folded target to form a probe/folded target complex; and
 - c) detecting said probe/folded target complex, thereby detecting the presence of said folded target in said sample.
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- B2
16. (AMENDED) A method for comparing the structure of nucleic acid targets, comprising:
- a) providing:
 - i) a first folded target having a nucleic acid sequence comprising first and second portions, said first and second portions each comprising one or more double stranded regions and one or more single stranded regions;
 - ii) a second folded target having a nucleic acid sequence comprising a first portion that is identical to said first portion of said first folded target and a second portion that differs from said second portion of said first folded target because of a variation in nucleic acid sequence relative to said first folded target, said first and second portions each comprising one or more double stranded regions and one or more single stranded regions;

- B2
- iii) first and second bridging oligonucleotides said first bridging oligonucleotide complementary to said first portion of said first and second folded targets and said second bridging oligonucleotide complementary to said second portion of said first and second folded targets; and
 - b) contacting said first folded target with said first bridging oligonucleotide under conditions such that said first bridging oligonucleotide binds to said first folded target to form a probe/folded target complex in a first mixture;
 - c) contacting said first folded target with said second bridging oligonucleotide under conditions such that said second bridging oligonucleotide binds to said first folded target to form a probe/folded target complex in a second mixture;
 - d) contacting said second folded target with said first bridging oligonucleotide to form a third mixture;
 - e) contacting said second folded target with said second bridging oligonucleotide to form fourth mixture; and
 - f) comparing the amount of probe/folded target complex in said first, second, third, and fourth mixtures.

- B3
21. (AMENDED) A method for analyzing folded nucleic acid targets, comprising:
- a) providing:
 - i) a first folded target having a nucleic acid sequence comprising first and second portions, wherein said first and second portions each comprise one or more double stranded regions and one or more single stranded regions;
 - ii) a second folded target having a nucleic acid sequence comprising a first portion that is identical to said first portion of said first folded target, and a second portion that differs from said second portion of said first folded target because of a variation in nucleic acid sequence relative to said first folded target, said first and second portions each comprising one or more double stranded regions and one or more single stranded regions;
 - iii) a solid support comprising comprising immobilized first and second bridging oligonucleotides, said first bridging oligonucleotide complementary to said first portion of said first

B3

and second folded targets and second bridging oligonucleotide complementary to said second portion of said first and second folded targets; and

- b) contacting said first and second folded targets with said solid support under conditions such that said first and second bridging oligonucleotides hybridize to said first folded target to form a probe/folded target complex; and
 - c) analyzing the amount of probe/folded target complex formed on said solid support at said first and second testing zones.
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